SEQUENCE LISTING

<110> Batard, Yannick
       Durst, Francis
       Schalk, Michel
       Werck-Reichhart, Daniele

<120> RECODING OF DNA SEQUENCES PERMITTING
       EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST

<130> A32000

<140> 09/158,767
<141> 1998-09-23

<150> FR 97-12094
<151> 1997-09-24

<160> 20

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 2261
<212> DNA
<213> Triticum aestivum

<400> 1

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cagcagaagc tgcgcgagga gatcgtcgcc gttctgggcg ccggcgtggc ggtgacggag     1080
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<210> 2
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 2
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<210> 3
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 3
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<210> 4
<211> 71
<212> DNA
<213> Triticum aestivum

<220>
<223> Synthetic primer

<400> 4
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gcggtgctgg c   71

<210> 5
<211> 143
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 5
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gctgtttttgg ctattgctgt tgctaaattg actggtaaaa gatttagatt gccaccaggt   120
ccatccggcg cccccatcgt cgg   143

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 6
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<210> 7
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Altered sequences

<400> 7

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cgcacccgca acgtcgtctt cgacatcttc accggcaagg acaggacat  ggtgttcacg   360
gtgtacggcg accactggcg caagatgcgg cggatcatga cggtgccctt cttcaccaac   420
aaggtggtgg cgcagaaccg cgtggggtgg gaggaggagg cccggctggt ggtggaggac   480
ctcaaggccg acccggcggc ggcgacggcg ggcgtggtgg tccgccgcag gctgcagctc   540
atgatgtaca acgacatgtt ccgcatcatg ttcgaccgcc ggttcgagag cgtggccgac   600
ccgctcttca accagctcaa ggcgctcaac gccgagcgca gcatcctctc ccagagcttc   660
gactacaact acggcgactt catccccgtc ctccgcccct tcctccgccg ctacctcaac   720
cgctgcacca acctcaagac caagcggatg aaggtgttcg aggaccactt cgtccagcag   780
cgcaaggagg cgttggagaa gacgggtgag atcaggtgcg ccatggacca catcctggaa   840
gccgaaagga agggcgagat caaccacgac aacgtcctct acatcgtcga gaacatcaac   900
gtcgcagcca tcgagacgac gctgtggtcg atcgagtggg gcctcgcgga gctggtgaac   960
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gtgcagaact tccagctgct gccgccgccg gggcaggaca agatcgacac caccgagaag  1440
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gcttaa                                                             1506

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     <211> 1506
     <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Altered sequences

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cccatcgtcg gcaactggct gcaggtcggc gacgacctca accaccgcaa cctgatgggc   180
ctggccaagc ggttcggcga ggtgttcctc ctccgcatgg gcgtccgcaa cctggtggtc   240
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gtgtacggcg accactggcg caagatgcgg cggatcatga cggtgccctt cttcaccaac   420
aaggtggtgg cgcagaaccg cgtggggtgg gaggaggagg cccggctggt ggtggaggac   480
ctcaaggccg acccggcggc ggcgacggcg ggcgtggtgg tccgccgcag gctgcagctc   540
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gactacaact acggcgactt catccccgtc ctccgcccct tcctccgccg ctacctcaac      720
cgctgcacca acctcaagac caagcggatg aaggtgttcg aggaccactt cgtccagcag      780
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gtcgcagcca tcgagacgac gctgtggtcg atcgagtggg gcctcgcgga gctggtgaac      960
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gagaaggccg tcgaggccca cggcaacgat ttccggttcg tgcccttcgg cgtcggccgc     1320
cggagctgcc ccgggatcat cctcgcgctg cccatcatcg gcatcacgct cggacgcctg     1380
gtgcagaact tccagctgct gccgccgccg gggcaggaca agatcgacac caccgagaag     1440
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ggttaa                                                                 1506
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<210> 9
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Altered sequences

<400> 9
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cccatcgtcg gcaactggct gcaggtcggc gacgacctca accaccgcaa cctgatgggc      180
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cgcacccgca acgtcgtctt cgacatcttc accggcaagg acaggacat ggtgttcacg       360
gtgtacggcg accactggcg caagatgcgg cggatcatga cggtgccctt cttcaccaac      420
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gactacaact acggcgactt catccccgtc ctccgcccct tcctccgccg ctacctcaac      720
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gcttaa                                                                1506


        <210> 10
        <211> 2181
        <212> DNA
        <213> Triticum aestivum

        <400> 10
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gggacgtggg cggtggtggt gtcggcggtg ccgcgtaca tggcgtggtt ctggcggatg        180
tcccgcgggc tgcgcgggcc gcgggtttgg cccgtgctcg cagcctgcc gggcctggtg        240
cagcacgccg aggacatgca cgagtggatc gccggcaacc tgcgccgcgc gggcggcacg       300
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32

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tattttgaa gatgattttt c                                                 2181


        <210> 11
        <211> 39
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Synthetic primer


        <400> 11
atatatggat ccatggaggt ggggacgtgg gcggtggtg                               39


        <210> 12
        <211> 150
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Synthetic primer

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atggcttggt tttggagaat gtctagaggt ttgagaggtc caagagtttg gccagttttg       120
ggttctttgc caggcctggt gcagcacgcc                                        150


        <210> 13
        <211> 42
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Synthetic primer


        <400> 13
tatatagaat tccttctacg cgcacggcgc tgtggcactt gc                           42


        <210> 14
        <211> 1626
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33

<212> DNA
<213> Artificial Sequence

<220>
<223> Altered sequences

<400> 14

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caccgcctga ccgtggcgcc gggccaccgc gtggagcaga agatgtcgct cacgctcttc    1500
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<210> 15
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered sequences

<400> 15

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Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
         35              40              45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg
     50              55              60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val
65              70              75                  80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
             85                  90                  95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
             100             105             110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
         115             120             125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
     130             135             140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145             150             155             160
Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg
             165             170             175
Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
             180             185             190
Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala
         195             200             205
Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
     210             215             220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn
225             230             235             240
Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His
             245             250             255
Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg
         260             265             270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
         275             280             285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
     290             295             300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn
305             310             315             320
His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu
             325             330             335
Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr

         340             345             350
```

Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
        355   360   365

Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
        370   375   380

Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385   390   395   400

Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
                405   410   415

Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
        420   425   430

Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu
        435   440   445

Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
    450   455   460

Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465   470   475   480

Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys
                485   490   495

Lys Pro Leu Glu Ala
                500

    <210> 16
    <211> 501
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Altered sequences

    <400> 16
Met Asp Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
 1   5   10   15

Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg
                20   25   30

Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
        35   40   45

Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg
    50   55   60

Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val
65   70   75   80

Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
                85   90   95

Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
                100   105   110

Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys

```
            115                      120                      125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
        130                      135                      140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145                      150                      155                      160
Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg
                    165                      170                      175
Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
                180                      185                      190
Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala
            195                      200                      205
Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
        210                      215                      220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn
225                      230                      235                      240
Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His
                    245                      250                      255
Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg
                    260                      265                      270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
                    275                      280                      285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
        290                      295                      300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn
305                      310                      315                      320
His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu
                    325                      330                      335
Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
                340                      345                      350
Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
            355                      360                      365
Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
        370                      375                      380
Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385                      390                      395                      400
Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
                    405                      410                      415
Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
                420                      425                      430
Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu
            435                      440                      445
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
        450                      455                      460
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465                      470                      475                      480
```

37

Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys
               485   490   495

Lys Pro Leu Glu Ala
              500

<210> 17
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Altered sequences

<400> 17
Met Asp Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
1   5   10   15
Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg
           20   25   30
Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
         35   40   45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg
      50   55   60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val
65   70   75   80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
             85   90   95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
          100   105   110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
         115   120   125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
   130   135   140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145   150   155   160
Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg
         165   170   175
Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
         180   185   190
Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala
         195   200   205
Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
210   215   220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn
225   230   235   240
Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His

```
                  245                    250                    255
Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg
                  260                    265                    270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
                  275                    280                    285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
305               290                    295                    300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn
305               310                    315                    320
His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu
                  325                    330                    335
Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
                  340                    345                    350
Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
                  355                    360                    365
Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
    370                    375                    380
Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385                    390                    395                    400
Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
                       405                    410                    415
Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
                  420                    425                    430
Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu
                  435                    440                    445
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
    450                    455                    460
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465                    470                    475                    480
Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys
                       485                    490                    495
Lys Pro Leu Glu Ala
                  500


    <210> 18
    <211> 501
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Altered sequences

    <400> 18
Met Asp Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
 1                 5                    10                    15
```

Ala Val Leu Ala Ile Ala Val Ala Lys Leu Thr Gly Lys Arg Phe Arg
            20   25   30
Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
        35   40   45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Leu Ala Lys Arg
    50   55   60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Val Arg Asn Leu Val Val
65   70   75   80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
            85   90   95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
            100   105   110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
    115   120   125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
    130   135   140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145   150   155   160
Leu Lys Ala Asp Pro Ala Ala Ala Thr Ala Gly Val Val Val Arg Arg
                165   170   175
Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
            180   185   190
Arg Arg Phe Glu Ser Val Ala Asp Pro Leu Phe Asn Gln Leu Lys Ala
            195   200   205
Leu Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
            210   215   220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Asn
225   230   235   240
Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Val Phe Glu Asp His
                245   250   255
Phe Val Gln Gln Arg Lys Glu Ala Leu Glu Lys Thr Gly Glu Ile Arg
            260   265   270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
    275   280   285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
    290   295   300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Leu Ala Glu Leu Val Asn
305   310   315   320
His Pro Glu Ile Gln Gln Lys Leu Arg Glu Glu Ile Val Ala Val Leu
                325   330   335
Gly Ala Gly Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
            340   345   350
Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
            355   360   365
Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr

40

```
            370                    375                    380
Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385                    390                    395                    400
Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
                405                    410                    415
Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
                420                    425                    430
Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu
                435                    440                    445
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
    450                    455                    460
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465                    470                    475                    480
Pro Gly Gln Phe Thr Asn Gln Ile Leu Lys His Ala Thr Ile Val Cys
                485                    490                    495
Lys Pro Leu Glu Ala
                500


    <210> 19
    <211> 541
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Altered sequences

    <400> 19
Met Glu Val Gly Thr Trp Ala Val Val Val Ser Ala Val Ala Ala Tyr
1               5                   10                  15
Met Ala Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val
                20                  25                  30
Trp Pro Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp
                35                  40                  45
Met His Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr
    50                  55                  60
Gln Thr Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu
65                  70                  75                  80
Val Thr Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala
                85                  90                  95
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg
                100                 105                 110
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu
            115                 120                 125
Ala Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg
    130                 135                 140
```

Thr Ala Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu
145   150   155   160

Pro Ile Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln
            165   170   175

Asp Leu Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe
         180   185   190

Gly Lys Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe
         195   200   205

Ala Ser Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile
     210   215   220

Phe Pro Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met
225   230   235   240

Glu Thr Thr Leu Thr Ser Ser Met Ala His Val Asp Gln Tyr Leu Ala
            245   250   255

Ala Val Ile Lys Lys Arg Lys Leu Glu Leu Ala Ala Gly Asn Gly Lys
         260   265   270

Cys Asp Thr Ala Ala Thr His Asp Asp Leu Leu Ser Arg Phe Met Arg
      275   280   285

Lys Gly Ser Tyr Ser Asp Glu Ser Leu Gln His Val Ala Leu Asn Phe
     290   295   300

Ile Leu Ala Gly Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe
305   310   315   320

Trp Leu Val Ser Thr His Pro Ala Val Glu Arg Lys Ile Val Arg Glu
          325   330   335

Leu Cys Ser Val Leu Ala Ala Ser Arg Gly Ala His Asp Pro Ala Leu
         340   345   350

Trp Leu Ala Glu Pro Phe Thr Phe Glu Glu Leu Asp Arg Leu Val Tyr
         355   360   365

Leu Lys Ala Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro
370   375   380

Glu Asp Ser Lys His Val Val Ala Asp Asp Tyr Leu Pro Asp Gly Thr
385   390   395   400

Phe Val Pro Ala Gly Ser Ser Val Thr Tyr Ser Ile Tyr Ser Ala Gly
            405   410   415

Arg Met Lys Gly Val Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu
         420   425   430

Arg Trp Leu Ser Ala Asp Gly Thr Lys Phe Glu Gln His Asp Ser Tyr
         435   440   445

Lys Phe Val Ala Phe Asn Ala Gly Pro Arg Val Cys Leu Gly Lys Asp
     450   455   460

Leu Ala Tyr Leu Gln Met Lys Asn Ile Ala Gly Ser Val Leu Leu Arg
465   470   475   480

His Arg Leu Thr Val Ala Pro Gly His Arg Val Glu Gln Lys Met Ser
            485   490   495

Leu Thr Leu Phe Met Lys Gly Gly Leu Arg Met Glu Val Arg Pro Arg

```
                500                    505                    510
Asp Leu Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala
            515                    520                    525
Ala Thr Ala Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala
            530                    535                    540
```

    <210> 20
    <211> 541
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Altered sequences

    <400> 20

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Met Glu Val Gly Thr Trp Ala Val Val Val Ser Ala Val Ala Ala Tyr
1               5                   10                  15
Met Ala Trp Phe Trp Arg Met Ser Arg Gly Leu Arg Gly Pro Arg Val
                20                  25                  30
Trp Pro Val Leu Gly Ser Leu Pro Gly Leu Val Gln His Ala Glu Asp
            35                  40                  45
Met His Glu Trp Ile Ala Gly Asn Leu Arg Arg Ala Gly Gly Thr Tyr
        50                  55                  60
Gln Thr Cys Ile Phe Ala Val Pro Gly Val Ala Arg Arg Gly Gly Leu
65                  70                  75                  80
Val Thr Val Thr Cys Asp Pro Arg Asn Leu Glu His Val Leu Lys Ala
                85                  90                  95
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Phe Trp His Gly Val Phe Arg
                100                 105                 110
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Leu
            115                 120                 125
Ala Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg
            130                 135                 140
Thr Ala Met Ser Arg Trp Val Ser Arg Ser Ile His Gly Arg Leu Leu
145                 150                 155                 160
Pro Ile Leu Ala Asp Ala Ala Lys Gly Lys Ala Gln Val Asp Leu Gln
                165                 170                 175
Asp Leu Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Ala Phe
            180                 185                 190
Gly Lys Asp Pro Glu Thr Leu Ala Gln Gly Leu Pro Glu Asn Glu Phe
            195                 200                 205
Ala Ser Ala Phe Asp Arg Ala Thr Glu Ala Thr Leu Asn Arg Phe Ile
            210                 215                 220
Phe Pro Glu Phe Leu Trp Arg Cys Lys Lys Trp Leu Gly Leu Gly Met
225                 230                 235                 240
```

```
Glu Thr Thr Leu Thr Ser Ser Met Ala His Val Asp Gln Tyr Leu Ala
                  245                 250                 255
Ala Val Ile Lys Lys Arg Lys Leu Glu Leu Ala Ala Gly Asn Gly Lys
            260             265                 270
Cys Asp Thr Ala Ala Thr His Asp Asp Leu Leu Ser Arg Phe Met Arg
        275             280             285
Lys Gly Ser Tyr Ser Asp Glu Ser Leu Gln His Val Ala Leu Asn Phe
    290             295             300
Ile Leu Ala Gly Arg Asp Thr Ser Ser Val Ala Leu Ser Trp Phe Phe
305             310             315                     320
Trp Leu Val Ser Thr His Pro Ala Val Glu Arg Lys Ile Val Arg Glu
            325             330                 335
Leu Cys Ser Val Leu Ala Ala Ser Arg Gly Ala His Asp Pro Ala Leu
            340             345             350
Trp Leu Ala Glu Pro Phe Thr Phe Glu Glu Leu Asp Arg Leu Val Tyr
    355             360             365
Leu Lys Ala Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro
    370             375             380
Glu Asp Ser Lys His Val Val Ala Asp Asp Tyr Leu Pro Asp Gly Thr
385             390             395             400
Phe Val Pro Ala Gly Ser Ser Val Thr Tyr Ser Ile Tyr Ser Ala Gly
            405             410             415
Arg Met Lys Gly Val Trp Gly Glu Asp Cys Leu Glu Phe Arg Pro Glu
            420             425             430
Arg Trp Leu Ser Ala Asp Gly Thr Lys Phe Glu Gln His Asp Ser Tyr
        435             440             445
Lys Phe Val Ala Phe Asn Ala Gly Pro Arg Val Cys Leu Gly Lys Asp
    450             455             460
Leu Ala Tyr Leu Gln Met Lys Asn Ile Ala Gly Ser Val Leu Leu Arg
465             470             475             480
His Arg Leu Thr Val Ala Pro Gly His Arg Val Glu Gln Lys Met Ser
            485             490             495
Leu Thr Leu Phe Met Lys Gly Gly Leu Arg Met Glu Val Arg Pro Arg
            500             505             510
Asp Leu Ala Pro Val Leu Asp Glu Pro Cys Gly Leu Asp Ala Gly Ala
        515             520             525
Ala Thr Ala Ala Ala Ala Ser Ala Thr Ala Pro Cys Ala
530             535                 540
```